



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Mparch_un n.a. - n.a. database search, using Smith-Waterman algorithm
on: Thu Aug 21 10:07:45 1997; Mparch time 876.69 Seconds
Tabular output not generated. 894.092 Million cell updates/sec

Title: >US-08-469-637A-1
(1-1527) from US08469637A.seq
Description: 1527 1 CGCCGAGCCCGCCCTCCAA.....TTCAGCTGAAAAA.....1527
Perfect Score: 1527
N.A. Sequence: GCGGCGCGCGCGCGAGGTT.....AAGTTGACCTTTT
Comp: GCGGCGCGCGCGCGAGGTT.....AAGTTGACCTTTT

Scoring table:
Gap 6
TABLE default

Nmatch STD : Dbase 0; Query 0
Searched: 707517 seqs, 256659390 bases x 2
Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
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99:EST99
EST-STS-TWO
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160:EST160 161:EST161 162:EST162 163:EST163 164:EST164
165:EST165 166:EST166 167:EST167 168:EST168 169:EST169
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

Statistics: Mean 11.463; Variance 1.911; scale 5.997

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	563	36.9	602	195	AA037313	zc52h03.r1 Homo sapien 0.00e+00
2	327	21.4	346	73	H88769	YW23912.r1 Homo sapie 0.00e+00
3	187	12.2	458	49	HUM366H09B	Human aorta cDNA 5'-e 0.00e+00
4	173	11.3	370	49	HUM345E08B	Human aorta cDNA 5'-e 0.00e+00
5	114	7.5	303	49	HUM365F01B	Human aorta cDNA 5'-e 2.56e-195
6	114	7.5	387	49	HUM365H11B	Human aorta cDNA 5'-e 2.56e-195
7	56	3.7	157	140	C02463	HUMG0012349, Human G 4.02e-65
8	24	1.6	504	5	T72414	YC72807.r1 Homo sapie 1.55e-06
9	23	1.5	344	61	H14106	YM2805.r1 Homo sapie 3.63e-05
10	23	1.5	442	5	T71938	YM67604.r1 Homo sapie 3.63e-05
11	23	1.5	470	2	T60480	YB95403.r1 Homo sapie 3.63e-05
12	21	1.4	222	53	R94906	YG39B08.r1 Homo sapie 1.36e-02
13	22	1.4	241	44	H37487	15616 Arabidopsis th 7.51e-04
14	22	1.4	253	129	HSC08E062	H. sapiens partial CD 1.36e-02
15	22	1.4	267	148	W10583	ma3f10.r1 Soares mou 7.51e-04
16	22	1.4	300	183	AA100384	zn46h08.r1 Stratagene 7.51e-04
17	22	1.4	301	48	HUM245F10B	Human aorta cDNA 5'-e 7.51e-04
18	21	1.4	325	65	H29337	YM60807.r1 Homo sapie 1.36e-02
19	21	1.4	325	112	ATRS3517	A. thaliana transcrib 1.36e-02
20	21	1.4	325	19	T54964	YD42803.r1 Homo sapie 1.36e-02
21	22	1.4	330	13	R1CC0437A	Rice cDNA, partial se 7.51e-04
22	22	1.4	339	88	H65000	YU66410.r1 Homo sapie 1.36e-02
23	22	1.4	360	164	C14856	Human fetal brain cDN 7.51e-04
24	21	1.4	362	5	T70903	YC49803.r1 Homo sapie 1.36e-02
25	21	1.4	380	187	AA142584	mq64e05.r1 Soares 2nd 1.36e-02
26	22	1.4	385	180	AA087288	mol1d06.r1 Life Tech 7.51e-04
27	22	1.4	387	109	HSDH23G03	H. sapiens partial CD 7.51e-04
28	21	1.4	395	5	T71079	YC50C04.r1 Homo sapie 1.36e-02
29	22	1.4	406	126	W76826	me79g11.r1 Soares mou 7.51e-04
30	21	1.4	408	41	R27233	YB33801.r1 Soares mou 1.36e-02
31	22	1.4	410	6	T74804	YC60004.r1 Homo sapie 7.51e-04
32	21	1.4	447	184	AA011021	ze34c01.s1 Soares ret 1.36e-02
33	21	1.4	450	131	N68886	TG58TZY39d10.r1 Toxop 1.36e-02
34	21	1.4	453	193	AA164719	z09f104.s1 Stratagene 1.36e-02
35	22	1.4	453	111	N21157	YX47d01.r1 Homo sapie 7.51e-04
36	21	1.4	465	193	AA164056	mt67g06.r1 Soares mou 1.36e-02
37	22	1.4	465	6	T77351	YD72810.r1 Homo sapie 7.51e-04
38	22	1.4	472	57	T42477	5740 Arabidopsis thal 7.51e-04
39	21	1.4	472	147	AA003244	mg44g01.r1 Soares mou 1.36e-02
40	21	1.4	478	172	AA061066	mj86h11.r1 Soares mou 1.36e-02
41	21	1.4	480	175	WB1931	me93c11.r1 Soares mou 1.36e-02
42	22	1.4	493	55	R1CS1559A	Rice cDNA, partial se 7.51e-04
43	21	1.4	500	94	N38845	YH80411.s1 Homo sapie 1.36e-02
44	22	1.4	796	117	W28026	55c10 Human retina CD 7.51e-04
45	21	1.4	798	115	W22001	6268 Human retina cDN 1.36e-02

ALIGNMENTS

RESULT 1
LOCUS AA037313 602 bp mRNA EST 25-NOV-1996
DEFINITION zc52h03.r1 Soares senescent fibroblasts NBHSF Homo sapiens CDNA
ACCESSION AA037313
NID G1512420
KEYWORDS EST.

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 602) Hillier,L., Clark,N., Dubucq,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Knudsen,T., Le M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R. The Mashu-Merck EST Project Unpublished (1995)
TITLE	Contact: Wilson RK
JOURNAL	Mashu-Merck EST Project
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information; Insert Length: 1203 Std Error: 0.00 Seq primer: -28M13 rev2 from AmerSham High quality sequence stop: 435. Location/Qualifiers 1..602 /organism="Homo sapiens" /note="vector: p717d (Pharmacia) with a modified polylinker V_type: phagemid; Site.1: Not I; Site.2: Eco RI; tcttaccattcgaacgtcgagccggccgcatTTTTTTTTTTT 3'1, double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p717 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Benito Soares and M.Fatima Bernaldo." /clone_id="325973" /clone_lib="Soares senescent fibroblasts NBHS" /lissue_type="senescent fibroblast" /lab_host="DH10B (ampicillin resistant)" <1...>602
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BASE COUNT	209 a. 128 c 136 g 126 t 3 others
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Query Match	36.9%; Score 563; DB 195; Length 602;
Best Local Similarity	98.7%; Pred. No. 0.00e+00;
"atches 588; Conservative	0; Mismatches 4; Indels 4; Gaps 4;
2	tctaagaaccttgtagaaacacacaatctgcgaagtcttttgcttcctgtaactca 61
511	tctTAAGACCCCTGTAGAAACAACAAT- GCAGTGCTTTGGTCTCCTGTAATCA 569
62	gaaggaaatccaacacacgcgaacatatgttccggaaaacagtgaatcaactcaaatg 121
570	GAAAGGAATGCACAACACGACACATATGTCGGAAAACGTAATCAACTCAAATG 629
122	tggaaatagatgttccctgtgtgtgaggagcaattctccaagttgttcgttccataaagt 181
630	TGGATAATATCTTACCCTGTGTGAGGAGCATTTCTACAGTTTCTTCTCTCAAAATT 689
182	tacgcccaacgttgtgtgtctgtgtagaaatttccctggcaccaaatgaagcaga 241
690	TACGCCCTACTGGCTTAGTGCTTTGGTAGAATAATTTCCCTGGCACCAATAAAGCGAGA 749
242	gagtgtagagagga laaaacygcaacacagctccaagaacacagacttccaagttcgtaa 301
750	GAGGTAGAGAGATAAACGCAACACAGCTCACAGAACAGACTTCCAGTGTGTGAA 809
302	gttatggaacaacaaaaaacagaccagaatatgttcaagaagaatcatccaagatatgga 361
810	GTATGGAACATCAAAAAACAAGACCAAGATATGTGTCAGAGAGATCATCCAGATATTTGA 869

Db	362	ccctctggaagaaacgcgtgcagagggcaccatttgtagacatctgctaacccttcgagcagc	421
QY	870	ccctctggaagaaacgcgtgcagagggcaccatttgtagacatctgctaacccttcgagcagc	928
Db	422	ttctgtagcttgtagaggaagcttaccgaggaagaaagttgtagagcagaagcattgaaaa	481
QY	929	tt-ctgtagcttgtagaggaagcttaccgaggaagaaagttgtagagcagaagcattgaaaa	987
Db	482	acaataaaggcatcacaaccacagtcagcagaatnctgtagcctgctcagcttctgtgcgata	541
QY	988	ACAATAAAGGATGCAAAACCAACGAGACGACATCCTGAGAGTGGCTGCACTTTGTGGCAGATA	1047
Db	542	aaaaatggcgaccaagaanaccttgtaaaaggngctaaycagcagcacttaagcactcaa	597
QY	1048	AAAAATGGCGACCAAGACACCTTGAA-GGGCCTTAATGACAGCACTAAGACATCAAA	1102
RESULT	2		
LOCUS	H88769	346 bp	MRNA
DEFINITION	Yw23g12.r1 Homo sapiens CDNA	253126 5'	
ACCESSION	H88769		
NID	91071029		
KEYWORDS	EST.		
SOURCE	human clone=253126 primer-M13RPI library-Morton Fetal Cochlea vector-Pbluscript SK- host-SOLR cells (Xenamycin resistant) Rait1-EORI Rait2-XhoI The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dr sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends. adaptor linker: GAATTGGCAGCG.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 346) Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Meria,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevasz,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.		
TITLE	Washu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 278 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers 1..346 /organism="Homo sapiens" /clone="253126"		
FEATURES	source		
BASE COUNT	104 a	71 c	62 g 106 t 3 others
ORIGIN	MRNA <1..346		
Query Match	21.4%	Score 327; DB 73; Length 346;	
Best Local Similarity	98.3%	Pred. No. 0.00e+00;	
Matches 340;	Conservative 0;	Mismatches 4;	Indels 2; Gaps 2;
Db	1	tcaggttccttcacagcttcacaaatgataatgatacagaagattatttagaataga	60
QY	1151	TCAGGTTCCTTCACAGCTTCACAAATGTAACAAATTGATCAGAAATTATTTTGAATGA	1210
Db	61	taggtaccgcggtcccaatcagtaataaagcgcgtattataacccggaatggccattggac	120
Y	1211	TAGGTACCGAGGTCCATCGTAAATAAGTGGCTTATTAACGTGAATGGCCATTGGAC	1270

TITLE
JOURNAL
COMMENT
Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
Tateuchi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y.,
Maekawa,H., Shin,S. and Nakamura,Y.
Unpublished (1995)
Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawachi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.

FEATURES
source
1..303
Location/Qualifiers
/organism="Homo sapiens"
/clone.lib="Clontech human aorta polyA+ mRNA (#6572)"

T. COUNT 102 a 54 c 37 g 106 t 4 others

IN

Query Match
Best Local Similarity 98.3%; Score 114; DB 49; Length 303;
Pred. No. 2,56e-195;
Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ctaacatctccccaataaaccacaatggttaatccaactgcatcgatcgatcgat 60
|||||
1410 CTACATCTCCCTCCCAATAAACCCCAATGGTTAATCCACTGCTGATCTGATCTAT 1469

Db 61 ctactgactatatttcccttattactgctgcatgtaattcaactggaataaaaa 118
|||||
2y 1470 CTACTGACTATATTTTCCCTTATTACTGCTGCACTGAATTCACATGGAATAAAAAA 1527

RESULT 6
LOCUS HUM366H1B 387 bp mRNA EST 29-AUG-1995
DEFINITION Human aorta CDNA 5'-end GEN-366H1.
ACCESSION D63126
NID g968051
KEYWORDS EST(expressed sequence tag); Human aorta; similar to none(May 29, 1995).
SOURCE Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))
CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 387)
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
Tateuchi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y.,
Maekawa,H., Shin,S. and Nakamura,Y.
Unpublished (1995)
TITLE Unpublished (1995) to DDBJ by:
JOURNAL Submitted (30-May-1995) to DDBJ by:
COMMENT Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawachi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.

FEATURES
source
1..387
Location/Qualifiers
/organism="Homo sapiens"
/clone.lib="Clontech human aorta polyA+ mRNA (#6572)"

BASE COUNT 135 a 62 c 50 g 140 t

ORIGIN

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Best Local Similarity 98.3%; Score 114; DB 49; Length 387;
Pred. No. 2,56e-195;
Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ctaacatctccccaataaaccacaatggttaatccaactgcatcgatcgatcgat 60
|||||
1410 CTACATCTCCCTCCCAATAAACCCCAATGGTTAATCCACTGCTGATCTGATCTAT 1469

Db 61 ctactgactatatttcccttattactgctgcatgtaattcaactggaataaaaa 118
|||||
2y 1470 CTACTGACTATATTTTCCCTTATTACTGCTGCACTGAATTCACATGGAATAAAAAA 1527

RESULT 7
LOCUS HUM366H1B 387 bp DNA EST 11-JUL-1996
DEFINITION Human Gene Signature, 3'-directed CDNA sequence.
ACCESSION C02463
NID g1434693
KEYWORDS Gene Signature; GS; EST(expressed sequence tag); BodyMap; gene expression.
SOURCE One or more human adult tissue.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 157)
Okubo,K.
Direct Submission
Submitted (28-DEC-1995) to the DDBJ/EMBL/GenBank databases. Kousaku
Okubo, Osaka University, Institute for Molecular and Cellular Bio;
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
(e-mail:kousaku@imcb.osaka-u.ac.jp, Tel:06-877-5111(ex.3315),
Fax:06-877-1922)
2 (bases 1 to 157)
Okubo,K.
BodyMap: human gene expression database
Unpublished (1995)
JOURNAL We are not submitting the same CDNA sequence redundantly to DDBJ
COMMENT since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
source
1..157
Location/Qualifiers
/organism="Homo sapiens"

BASE COUNT 46 a 26 c 24 g 54 t 7 others

ORIGIN

Query Match
Best Local Similarity 95.5%; Score 56; DB 140; Length 157;
Pred. No. 4.02e-65;
Matches 64; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Db 1 gatcgatattctgactatatttccctgattactgctgcatgtaattcaactgga 60
|||||
1461 GATCGTATCTACTGACTATATTTCCCT-TATTACTGCTGCGATTCACACTGAAA 1519

Db 61 ttaaaa 67
|||||

2y 1520 AAAAAA 1526

RESULT 8
LOCUS T72414 504 bp mRNA EST 01-MAR-1995
DEFINITION yc72407.r1 Homo sapiens CDNA clone 86196 5' similar to
gp:K54486.rnal PLASMA PROTEASE CI INHIBITOR PRECURSOR (HUMAN);
ACCESSION T72414
NID g686935
KEYWORDS EST.
SOURCE human clone=86196 library=Stratagene liver (#937224)
vector=PB1uescript SK host=SOBR cells (kanamycin resistant)
primer-M13R1 Rsite1-EcoRI Rsite2-XhoI Cloned unidirectionally.
Primer: Oligo dT. Hepatectomy from normal 49 year old male
caucasian. Average insert size: 1.1 kb; Uni-TAP XR Vector: 5'
adaptor sequence: 5'-GAATTCGCGACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTATTTTATTTTATTTT-3'.

Query Match 1.4% Score 22; DB 148; Length 267;
 Best Local Similarity 75.0%; Pred. No. 7.51e-04;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

3b 31 gaagctgctggaagcgagagagcatgattctctgctctgc 74
 |||||
 3p 931 GAAGCTGCTCGAAGCTGAGGTAGCATGTCCAAATGTGCCCTGC 888

Search completed: Thu Aug 21 10:35:06 1997
 Job time : 1641 secs.